



SEQUENCE LISTING

<110> Anderson, John P.
Basi, Gurigbal
Doane, Minh Tam
Frigon, Normand
John, Varghese
Power, Michael
Sinha, Sukanto
Tatsuno, Gwen
Tung, Jay
Wang, Shuwen
McConlogue, Lisa

<120> Beta-Secretase Enzyme Compositions and
Methods

<130> 228-US-NEW2C4

<140> US 09/724,571

<141> 2000-11-28

<150> US 09/501,708

<151> 2000-02-10

<150> 60/119,571

<151> 1999-02-10

<150> 60/139,172

<151> 1999-06-15

<160> 104

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 1

atggcccaag	ccctgccctg	gctcctgctg	tggatgggag	cgggagtgct	gcctgccac	60
ggcaccacag	acggcatccg	gctgccctg	cgcagcggcc	tgggggggag	ccccctggg	120
ctgcggctgc	cccgggagac	cgacgaagag	cccaggagag	ccggccggag	gggcagcttt	180
gtggagatgg	tggacaacct	gaggggcaag	tcggggcagg	gctactacgt	ggagatgacc	240
gtgggcagcc	ccccgcagac	gctcaacatc	ctgggtggata	caggcagcag	taactttgca	300
gtgggtgctg	ccccccaccc	cttcctgcat	cgctactacc	agaggcagct	gtccagcaca	360
taccgggacc	tccggaagg	tgtgtatgtg	ccctacaccc	agggcaagt	ggaaggggag	420
ctgggcaccg	acctggtaag	catcccccat	ggccccacg	tactgtgctg	tgccaacatt	480
gctgccatca	ctgaatcaga	caagtctctc	atcaacggct	ccaactggga	aggcatcctg	540
gggctggcct	atgctgagat	tgccaggcct	gacgactccc	tggagccttt	ctttgactct	600
ctggtaaagc	agaccacagt	tcccaacctc	ttctccctgc	agctttgtgg	tgctggcttc	660
cccctcaacc	agtctgaagt	gctggcctct	gtcggaggga	gcatgatcat	tggagggtatc	720
gaccactcgc	tgtacacagg	cagtctctgg	tatacaccca	tccggcggga	gtggtattat	780
gaggtgatca	ttgtgctggg	ggagatcaat	ggacaggatc	tgaataggga	ctgcaaggag	840
tacaactatg	acaagagcat	tgtggacagt	ggcaccacca	accttcggtt	gccaagaaa	900
gtgtttgaag	ctgcagtcaa	atccatcaag	gcagcctcct	ccacggagaa	gttccttgat	960
ggttttctgg	taggagagca	gctgggtgtg	tggcaagcag	gcaccacccc	ttggaacatt	1020
ttcccagtc	tctcactcta	cctaattggg	gaggttacca	accagtcctt	ccgcatcacc	1080
atccttccgc	agcaatacct	gcggccagtg	gaagatgtgg	ccacgtccca	agacgactgt	1140

```
<210> 2
<211> 501
<212> PRT
<213> Homo sapiens
```

Met 1	Ala	Gln	Ala	Leu 5	Pro	Trp	Leu	Leu	Leu 10	Trp	Met	Gly	Ala	Gly 15	Val
Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser
		20					25					30			
Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
		35					40					45			
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
	50					55					60				
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
65					70					75					80
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
				85					90					95	
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
			100				105					110			
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
		115					120					125			
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp
	130					135					140				
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile
145					150					155					160
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp
				165					170					175	
Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp
			180					185					190		
Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro
		195					200					205			
Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln
	210					215					220				
Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile
225					230					235					240
Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg
				245					250					255	
Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln
			260					265					270		
Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val
		275					280					285			
Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala
	290					295					300				
Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp
305					310					315					320
Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr
				325					330					335	
Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val
			340					345					350		
Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg

370	375	380
Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu		
385	390	395
Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala		400
	405	410
Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu		415
	420	425
Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro		430
	435	440
Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala		445
	450	455
Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp		460
465	470	475
Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp		480
	485	490
Ile Ser Leu Leu Lys		495
500		

<210> 3
 <211> 24
 <212> DNA
 <213> Homo sapiens

<400> 3
 gagagacgar garccwgagg agcc

24

<210> 4
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 4
 gagagacgar garccwgaag agcc

24

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 5
 gagagacgar garccwgaag aacc

24

<210> 6
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 6
 gagagacgar garccwgagg aacc

24

<210> 7
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 7
 agagacgarg arccsgagga gcc 23

<210> 8
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 8
 agagacgarg arccsgaaga gcc 23

<210> 9
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 9
 agagacgarg arccsgaaga acc 23

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 10
 agagacgarg arccsgagga acc 23

<210> 11
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 11
 cgtcacagrt trtcaaccat ctc 23

<210> 12
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 12
 cgtcacagrt trtctacat ctc 23

<210> 13
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 13
 cgtcacagrt trtccacat ctc 23

<210> 14
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 14
 cgtcacagrt trtcgacat ctc 23

<210> 15
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 15
 cgtcacagrt trtcaacat ttc 23

<210> 16
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 16
 cgtcacagrt trtctacat ttc 23

<210> 17

<211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 17
 cgtcacagrt trtccaccat ttc

23

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 18
 cgtcacagrt trtcgaccat ttc

23

<210> 19
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 19
 gaggggcagc tttgtggaga

20

<210> 20
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 20
 cagcataggc cagccccagg atgcct

26

<210> 21
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer derived from SEQ
 ID NO: 2

<400> 21
 gtgatggcag caatgttggc acgc

24

<210> 22
 <211> 17

1040754250

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 22
 gaygargagc cngagga 17

<210> 23
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 23
 gaygargagc cngaaga 17

<210> 24
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 24
 gaygargaac cngagga 17

<210> 25
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<221> misc_feature
 <222> (1)...(17)
 <223> n = A,T,C or G

<400> 25
 gaygargaac cngaaga 17

<210> 26
 <211> 15
 <212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc_feature

<222> (1)...(15)

<223> n = A,T,C or G

<400> 26

rttrtcnacc atttc

15

<210> 27

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc_feature

<222> (1)...(15)

<223> n = A,T,C or G

<400> 27

rttrtcnacc atctc

15

<210> 28

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 28

tcnaccatyt cnacaaa

17

<210> 29

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 29

tcnaccatyt cnacgaa

17

<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<400> 30
 atattctaga gaygargagc cagaaga 27

<210> 31
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<400> 31
 atattctaga gaygargagc cggaaga 27

<210> 32
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<400> 32
 atattctaga gaygargagc ccgaaga 27

<210> 33
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<400> 33
 atattctaga gaygargagc ctgaaga 27

<210> 34
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<221> misc_feature
 <222> (1)...(30)
 <223> n = A,T,C or G

<400> 34
 acacgaattc ttrtcnacca tytcaacaaa 30

<210> 35
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc_feature

<222> (1)...(30)

<223> n = A,T,C or G

<400> 35

acacgaattc ttrtcnacca tytcgacaaa

30

<210> 36

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc_feature

<222> (1)...(30)

<223> n = A,T,C or G

<400> 36

acacgaattc ttrtcnacca tytccacaaa

30

<210> 37

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc_feature

<222> (1)...(30)

<223> n = A,T,C or G

<400> 37

acacgaattc ttrtcnacca tytctacaaa

30

<210> 38

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<400> 38

aagagcccgg ccggaggggc a

21

<210> 39

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<400> 39

aaagctgccc ctccggccgg g

21

2025-04-26

<210> 40
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<400> 40
 agctcgttta gtgaaccgtc agatcg

26

<210> 41
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate oligonucleotide primer

<400> 41
 acctacaggt ggggtctttc attccc

26

<210> 42
 <211> 2348
 <212> DNA
 <213> Homo sapiens

<400> 42
 ccattgccggc ccctcacagc cccgccggga gcccgagccc gctgcccagg ctggccggccg 60
 csgtgccgat gtagcgggct ccggatccca gcctctcccc tgctcccgtg ctctgcggat 120
 ctcccctgac cgctctccac agcccggacc cgggggctgg cccaggggccc tgcaggccct 180
 ggcgtcctga tgcccccaag ctccctctcc tgagaagcca ccagcaccac ccagacttgg 240
 gggcaggcgc cagggacgga cgtgggccag tgcgagccca gagggcccga aggccggggc 300
 ccaccatggc ccaagccctg ccctggctcc tgctgtggat gggcgccggga gtgctgcctg 360
 cccacggcac ccagcacggc atccggctgc ccctgcgcag cggcctgggg ggcgcccccc 420
 tggggctgcg gctgccccgg gagaccgacg aagagcccga ggagcccggc cggaggggca 480
 gctttgtgga gatggtggac aacctgaggg gcaagtccgg gcagggtac tacgtggaga 540
 tgaccgtggg cagccccccg cagacgctca acatcctggg ggatacaggc agcagtaact 600
 ttgcagtggg tgctgcccc caccctctcc tgcacgcta ctaccagagg cagctgtcca 660
 gcacataccg ggacctccgg aagggtgtgt atgtgcccta caccagggc aagtgggaag 720
 gggagctggg caccgacctg gtaagcatcc cccatggccc caacgtcact gtgcgtgcca 780
 acattgctgc catcactgaa tcagacaagt tcttcacaa cggctccaac tgggaaggca 840
 tcctggggct ggcctatgct gagattgcca ggctgacga ctccctggag cctttctttg 900
 actctctggt aaagcagacc caggttccca acctcttctc cctgcagctt tgtggtgctg 960
 gcttccccct caaccagtct gaagtgtggt cctctgtcgg agggagcatg atcattggag 1020
 gtatcgacca ctgctgttac acaggcagtc tctggtatac accatccgg cgggagtggg 1080
 attatgaggt gatcattgtg cgggtggaga tcaatggaca ggatctgaaa atggactgca 1140
 aggagtacaa ctatgacaag agcattgtgg acagtggcac caccaacctt cgtttgcccc 1200
 agaaagtgtt tgaagctgca gtcaaatcca tcaaggcagc ctccctccacg gagaagttcc 1260
 ctgatggttt ctggctagga gagcagctgg tgtgctggca agcaggcacc accccttgga 1320
 acattttccc agtcatctca ctctacctaa tgggtgaggt taccaaccag tccttccgca 1380
 tcaccatcct tccgcagcaa tacctgcccc cagtgggaaga tgtggccacg tcccaagacg 1440
 actgttacaa gtttgccatc tcacagtcac ccacgggcac tgttatggga gctgttatca 1500
 tggagggtct ctacgttgct tttgatcggg ccgaaaaacg aattggcttt gctgtcagcg 1560
 cttgccatgt gcacgatgag ttcaggacgg cagcgggtga aggccctttt gtcaccttgg 1620
 acatggaaga ctgtggctac aacattccac agacagatga gtcaaccctc atgaccatag 1680
 cctatgtcat ggctgccatc tgcgccctct tcatgctgcc actctgcctc atggtgtgtc 1740
 agtggcgctg cctccgctgc ctgcgccagc agcatgatga ctttgcctgat gacatctccc 1800
 tgctgaagtg aggaggccca tgggcagaag atagagattc ccctggacca cacctccgtg 1860
 gttcactttg gtcacaagta ggagacacag atggcacctg tggccagagc acctcaggac 1920
 cctccccacc caccaaatgc ctctgccttg atggagaagg aaaaggctgg caagggtggg 1980

```

tccaggggact gtacctgtag gaaacagaaa agagaagaaa gaagcactct gctggcgggg 2040
atactcttgg tcacctcaaa ttttaagtcgg gaaattctgc tgcttgaaac ttcagccctg 2100
aacctttgtc caccattcct ttaaattctc caacccaaag tattcttctt ttcttagttt 2160
cagaagtact ggcacacac gcaggttacc ttggcgtgtg tcctgtgggt accctggcag 2220
agaagagacc aagcttgttt cctgtctggc caaagtcagt aggagaggat gcacagtttg 2280
ctatttgctt tagagacagg gactgtataa acaagcctaa cattgggtgca aagattgcct 2340
cttgaatt 2348

```

```

<210> 43
<211> 456
<212> PRT
<213> Homo sapiens

```

```

<400> 43
Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1      5      10      15
Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val
20     25     30
Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
35     40     45
Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
50     55     60
His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
65     70     75     80
Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
85     90     95
Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg
100    105    110
Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
115    120    125
Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg
130    135    140
Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr
145    150    155    160
His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro
165    170    175
Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile
180    185    190
Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro
195    200    205
Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile
210    215    220
Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys
225    230    235    240
Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val
245    250    255
Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys
260    265    270
Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala
275    280    285
Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met
290    295    300
Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln
305    310    315    320
Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr
325    330    335
Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val
340    345    350
Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
355    360    365
Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala

```

370 375 380
 Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr
 385 390 395 400
 Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val
 405 410 415
 Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val
 420 425 430
 Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe
 435 440 445
 Ala Asp Asp Ile Ser Leu Leu Lys
 450 455

<210> 44
 <211> 2348
 <212> DNA
 <213> Homo sapiens

<400> 44
 ccatgccggc ccctcacagc cccgccggga gcccagagccc gctgcccagg ctggccgccc 60
 csagtgcgat gtagcgggct ccggatccca gcctctcccc tgctcccgtg ctctgcggat 120
 ctcccctgac cgctctccac agcccggacc cgggggctgg ccaggggccc tgcaggccct 180
 ggcgtcctga tgcctccaag ctccctctcc tgagaagcca ccagcaccac ccagacttgg 240
 gggcaggcgc caggagcggg cgtggggccag tgcgagccca gagggcccga aggcgggggc 300
 ccaccatggc ccaagccctg ccctgggtcc tgctgtggat gggcgccgga gtgctgcctg 360
 cccacggcac ccagcacggc atccgggtgc ccctgcgcag cggcctgggg ggcgcccccc 420
 tggggctgcg gctgccccgg gagaccgacg aagagcccga ggagcccggc cggaggggca 480
 gctttgtgga gatggtggac aacctgaggg gcaagtcggg gcagggctac tacgtggaga 540
 tgaccgtggg cagccccccg cagacgtca acatcctggt ggatacaggc agcagtaact 600
 ttgcagtggg tgctgcccc caccctctcc tgcacgccta ctaccagagg cagctgtcca 660
 gcacataccg ggacctccgg aagggtgtgt atgtgcccta caccagggc aagtgggaag 720
 gggagctggg caccgacctg gtaagcatcc cccatggccc caacgtcact gtgcgtgcca 780
 acattgtctc catcactgaa tcagacaagt tcttcatcaa cggctccaac tgggaaggca 840
 tcctggggct ggcctatgct gagattgcca ggctgacga ctccctggag cctttctttg 900
 actctctggt aaagcagacc cacgttccca acctcttctc cctgcagctt tgtggtgctg 960
 gcttccccct caaccagtct gaagtgtcgg cctctgtcgg agggagcatg atcattggag 1020
 gtatcgacca ctgcgtgtac acaggcagtc tctggtatac acccatccgg cgggagtggt 1080
 attatgaggt gatcattgtg cgggtggaga tcaatggaca ggatctgaaa atggactgca 1140
 aggagtacaa ctatgacaag agcattgtgg acagtggcac caccaacctt cgtttgcccc 1200
 agaaagtgtt tgaagctgca gtcaaatacca tcaaggcagc ctctccacg gagaagttcc 1260
 ctgatggttt ctggctagga gagcagctgg tgtgctggca agcaggcacc accccttgga 1320
 acattttccc agtcatctca ctctacctaa tgggtgaggt taccaaccag tccttccgca 1380
 tcaccatcct tccgcagcaa tacctgcggc cagtggaaga tgtggccacg tcccaagacg 1440
 actgtttaca gtttgccatc tcacagtcac ccacgggcac tgttatggga gctgttatca 1500
 tggagggctt ctacgttgtc tttgatcggg cccgaaaacg aattggcttt gctgtcagcg 1560
 cttgccatgt gcacgatgag ttcaggacgg cagcggtgga aggccctttt gtcaccttg 1620
 acatggaaga ctgtggctac aacattccac agacagatga gtcaaccctc atgaccatag 1680
 cctatgtcat ggctgccatc tgcgccctct tcatgctgcc actctgcctc atggtgtgtc 1740
 agtggcgctg cctccgctgc ctgcgccagc agcatgatga ctttgcctgat gacatctccc 1800
 tgctgaagtg aggaggccca tgggcagaag atagagattc ccctggacca cacctccgtg 1860
 gttcactttg gtcacaagta ggagacacag atggcacctg tggccagagc acctcaggac 1920
 cctccccacc caccaaatgc ctctgccttg atggagaagg aaaaggctgg caaggtgggt 1980
 tccaggggact gtacctgtag gaaacagaaa agagaagaaa gaagcactct gctggcgggg 2040
 atactcttgg tcacctcaaa tttaagtcgg gaaattctgc tgcttgaaac ttcagccctg 2100
 aacctttgtc caccattcct ttaaattctc caacccttct tttcttctt ttcttagttt 2160
 cagaagtact ggcattcacac gcaggttacc ttggcgtgtg tccctgtggt accctggcag 2220
 agaagagacc aagcttggtt cctgtctggc caaagtcagt aggagaggat gcacagtttg 2280
 ctatttgctt tagagacagg gactgtataa acaagcctaa cattggtgca aagattgcct 2340
 cttgaatt 2348

<210> 45
 <211> 7

094531.0401

<212> PRT
<213> Artificial Sequence

<220>
<223> Flag sequence

<400> 45
Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 46
<211> 22
<212> PRT
<213> Homo sapiens

<400> 46
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15
Leu Pro Ala His Gly Thr
20

<210> 47
<211> 23
<212> PRT
<213> Homo sapiens

<400> 47
Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro
1 5 10 15
Leu Gly Leu Arg Leu Pro Arg
20

<210> 48
<211> 16080
<212> DNA
<213> Artificial Sequence

<220>
<223> Expression Vector pCEK

<221> misc_feature
<222> (1)...(16080)
<223> n = A,T,C or G

<400> 48
ttctcatgtt tgacagctta tcatcgcaga tccgggcaac gttgttgcatt tgctgcaggc 60
gcagaactgg taggtatgga agatccgatg tacggggccag atatacgctg tgacattgat 120
tattgactag ttattaatag taatcaatta cgggggtcatt agttcatagc ccatatatgg 180
agttccgctg tacataactt acggtaaagt gcccgcctgg ctgaccgccc aacgaccccc 240
gccattgac gtcaataatg acgtatgttc ccatagtaac gccaataggg actttccatt 300
gacgtcaatg ggtggactat ttacggtaaa ctgcccactt ggagctacat caagtgtatc 360
atatgccaag tacgccccct attgacgtca atgacggtaa atggcccgcg tggcattatg 420
cccagtacat gaccttatgg gactttccta cttggcagta catctacgta ttagtcatcg 480
ctattaccat ggtgatgcgg ttttggcagt acatcaatgg gcgtggatag cggtttgact 540
cacggggatt tccaagtctc caccacattg acgtcaatgg gagtttgatt tggcaccaaa 600
atcaacggga ctttccaaaa tgtcgttaaca actccgcccc attgacgcaa atgggaggta 660
ggcgtgtacg gtgggaggtc tatataagca gagctctctg gctaactaga gaaccactg 720
cttactggct tatcgaaatt aatacgactc actataggga gacccaagct ctggtgggct 780
cgcggttgag gacaaactct tcgcggtctt tccagtactc ttggatcgga aaccgcgcg 840
cctccgaacg gtactccgcc accgagggac ctgagcagat ccgcatcgac cggatcgga 900
aacctctcga ctgttggggg gagtactccc tctcaaaagc gggcatgact tctgcgctaa 960

092454.0104

gattgtcagt	ttccaaaaaac	gaggaggatt	tgatattcac	ctggcccgcg	gtgatgcctt	1020
tgaggggtggc	cgcgtccatc	tggtcagaaa	agacaatctt	tttgttgtca	agcttgaggt	1080
gtggcaggct	tgagatctgg	ccatacactt	gagtgacaat	gacatccact	ttgcctttct	1140
ctccacaggt	gtccactccc	aggtccaact	gcaggctgac	tctagaccgc	gggaattctg	1200
cagatatcca	tcacactggc	cgcactcgtc	cccagcccgc	ccgggagctg	cgagccgcga	1260
gctggattat	ggtggcctga	gcagccaacg	cagccgcagg	agcccggagc	ccttgcccct	1320
gcccgcgcgc	ccgcccgcgc	gggggaccag	ggaagccgcc	accggcccgc	catgcccgcc	1380
cctcccagcc	ccgcccggag	cccgcgcccg	ctgcccaggc	tggccgcgcg	cgtgccgatg	1440
tagcgggctc	cggatcccg	cctctcccct	gctcccgtgc	tctgoggatc	tcccctgacc	1500
gctctccaca	gcccgcaccc	gggggctggc	ccagggccct	gcaggccctg	gcgtcctgat	1560
gccccaaagc	tccctctcct	gagaagccac	cagcaccacc	cagacttggg	ggcaggcgcc	1620
agggacggac	gtgggcccagt	gcgagcccag	agggcccga	ggccgggggc	caccatggcc	1680
caagccctgc	cctggctcct	gctgtggatg	ggcgcgggag	tgtgcctgc	ccacggcacc	1740
cagcacggca	tccggctgcc	cctgcgcagc	ggcctggggg	gcgccccctt	ggggctgcgg	1800
ctgccccggg	agaccgacga	agagcccag	gagcccggcc	ggaggggcag	ctttgtggag	1860
atggtggaca	acctgagggg	caagtccggg	cagggtact	acgtggagat	gaccgtgggc	1920
agccccccgc	agacgctcaa	catcctgggt	gatacaggca	gcagtaactt	tgcagtgggt	1980
gctgcccccc	accccttcc	gcacgcgtac	taccagaggc	agctgtccag	cacataccgg	2040
gacctccgga	aggggtgtga	tgtgccttac	acccagggca	agtgggaagg	ggagctgggc	2100
accgacctgg	taagcatccc	ccatggcccc	aacgtcactg	tgcgtgccaa	cattgctgcc	2160
atcactgaat	cagacaagtt	cttcatcaac	ggctccaact	gggaaggcat	cctggggctg	2220
gcctatgctg	agattgccag	gcctgacgac	tccctggagc	ctttctttga	ctctctggta	2280
aagcagaccc	acgttcccaa	cctctttctc	ctgcagcttt	gtggtgctgg	cttccccctc	2340
aaccagtctg	aagtgctggc	ctctgtcggg	gggagcatga	tcatggagg	tatcgaccac	2400
tcgctgtaca	caggcagtct	ctggtataca	cccatccggc	gggagtggta	ttatgaggtc	2460
atcattgtgc	gggtggagat	caatggacag	gatctgaaaa	tggactgcaa	ggagtacaac	2520
tatgacaaga	gcattgtgga	cagtggcacc	accaaccctc	gtttgcccga	gaaagtgttt	2580
gaagctgcag	tcaaattccat	caaggcagcc	tcctccacgg	agaagtcccc	tgatggtttc	2640
tggctaggag	agcagctggt	gtgctggcaa	gcaggcacca	ccccttggaa	cattttccca	2700
gtcatctcac	tctaccta	gggtgaggtt	accaaccagt	ccttcgcgat	caccatcctt	2760
ccgcagcaat	acctgcggcc	agtggagat	gtggccacgt	cccaagacga	ctgttacaag	2820
tttgccatct	cacagtcac	cacgggcact	gttatgggag	ctgttatcat	ggagggcttc	2880
tacgttgtct	ttgatcgggc	ccgaaaacga	attggctttg	ctgtcagcgc	ttgccatgtg	2940
cacgatgagt	tcaggacggc	agcgggtggaa	ggcccttttg	tcaccttgga	catggaagac	3000
tgtggctaca	acattccaca	gacagatgag	tcaaccctca	tgaccatagc	ctatgtcatg	3060
gctgccatct	gcgcctctt	catgctgcca	ctctgctcca	tgggtgtgtca	gtggcgctgc	3120
ctccgctgcc	tgcgccagca	gcattgatgac	tttgcgtgat	acatctccct	gctgaagtga	3180
ggaggcccat	gggcagaaga	tagagattcc	cctggaccac	acctccgtgg	ttcacttttg	3240
tcacaagtag	gagacacaga	tggcacctgt	ggccagagca	cctcaggacc	ctccccacc	3300
accaaagtc	tctgccttga	tggagaagga	aaaggctggc	aagggtgggt	ccagggactg	3360
tacctgtagg	aaacagaaaa	gagaagaaag	aagcactctg	ctggcgggaa	tactcttggt	3420
cacctcaaat	ttaagtccgg	aaattctgct	gcttgaaact	tcagccctga	acctttgtcc	3480
accattcctt	taaattctcc	aacccaaagt	attcttcttt	tcttagtttc	agaagtactg	3540
gcacacacg	caggttacct	tggcgtgtgt	ccctgtggta	ccctggcaga	gaagagacca	3600
agcttgtttc	cctgctggcc	aaagtcagta	ggagaggatg	cacagtttgc	tatttgcttt	3660
agagacaggg	actgtataaa	caagcctaac	attggtgcaa	agattgcctc	ttgaattaaa	3720
aaaaaaaaact	agattgacta	tttatataaaa	tgggggcggc	tggaaagagg	agaaggagag	3780
ggagtacaaa	gacagggaat	agtgggatca	aagctaggaa	aggcagaaac	acaaccactc	3840
accagtccta	gttttagacc	tcatctccaa	gatagcatcc	catctcagaa	gatgggtgtt	3900
gttttcaatg	ttttcttttc	tgtggttgca	gcctgaccaa	aagtgagatg	ggaagggtt	3960
atctagccaa	agagctcttt	tttagctctc	ttaaatgaag	tgcccactaa	gaagttccac	4020
ttaacacatg	aatttctgcc	atattaattt	cattgtctct	atctgaacca	ccctttattc	4080
tacatatgat	aggcagcact	gaaatatcct	aaccccttaa	gtccagggtg	ccctgtggga	4140
gagcaactgg	actatagcag	ggctgggctc	tgttctctcg	gtcataggct	cactctttcc	4200
cccaaactctt	cctctggagc	tttgccagcca	aggtgctaaa	aggaataggt	aggagacctc	4260
ttctatctaa	tccttaaaag	cataatgttg	aacattcatt	caacagctga	tgcctataaa	4320
cccctgcctg	gatttcttcc	tattaggcta	taagaagtag	caagatcttt	acataattca	4380
gagtggtttc	attgccttcc	tacctctctc	aatggccctc	ccatttatctt	gactaaagca	4440
tcacacagtg	gcactagcat	tataccaaga	gtatgagaaa	tacagtgcct	tatggctcta	4500
acattactgc	cttcagtatc	aaggctgcct	ggagaaagga	tggcagcctc	agggcttcc	4560
tatgtcctcc	accacaagag	ctccttgatg	aaggctcatc	ttttccctta	tcctgttctt	4620

ccccccccg	ctcctaattg	tacgtgggta	cccaggctgg	ttcttgggct	aggtagtg	4680
gaccaagtgc	attacctccc	tatcagttct	agcatagtaa	actacggtag	cagtgttagt	4740
gggaagagct	gggttttcc	agtataccca	ctgcaccta	ctcctacctg	gtcaacccgc	4800
tgcttccagg	tatgggacct	gctaagtgtg	gaattacctg	ataagggaga	gggaaataca	4860
aggagggcct	ctggtgttcc	tggectcagc	cagctgcca	caagccataa	accaataaaa	4920
caagaatact	gagtcagttt	tttatctggg	ttctcttcat	tcccactgca	cttggtgctg	4980
ctttggctga	ctgggaacac	cccataacta	cagagtctga	caggaagact	ggagactgtc	5040
cacttctagc	tcggaactta	ctgtgtaaat	aaactttcag	aactgctacc	atgaagtga	5100
aatgccacat	tttgctttat	aattttctacc	catgttggga	aaaactggct	ttttccagc	5160
cctttccagg	gcataaaact	caaccccttc	gatagcaagt	cccatcagcc	tattattttt	5220
ctaaagaaaa	cttgcaacttg	tttttctttt	tacagttact	tccttcctgc	cccaaaatta	5280
taaactctaa	gtgtaaaaaa	aagtcttaac	aacagcttct	tgcttgtaaa	aatatgtatt	5340
atacatctgt	attttttaaat	tctgtctctg	aaaaatgact	gtcccattct	ccactcactg	5400
catttggggc	ctttccatt	ggtctgcatg	tcttttatca	ttgcaggcca	gtggacagag	5460
ggagaaggga	gaacaggggt	cgccaacact	tgtgttgctt	tctgactgat	cctgaacaag	5520
aaagagtaac	actgaggcgc	tcgctcccat	gcacaactct	ccaaaacact	tatcctcctg	5580
caagagtggg	ctttccgggt	ctttactggg	aagcagttaa	gccccctcct	caccccttcc	5640
ttttttcttt	ctttactcct	ttggttcaa	aggatttttg	aaaagaaaca	atatgcttta	5700
cactcatttt	caattttctaa	atttgcaggg	gatactgaaa	aatacggcag	gtggcctaag	5760
gtgctgtaa	agttgagggg	agaggaaatc	ttaagattac	aagataaaaa	acgaatcccc	5820
taaacaaaaa	gaacaataga	actgtcttcc	catttttgcca	cctttcctgt	tcatgacagc	5880
tactaacctg	gagacagtaa	catttccatta	accaaagaaa	gtgggtcacc	tgacctctga	5940
agagctgagt	actcaggcca	ctccaatcac	cctacaagat	gccaaggagg	tcccaggaag	6000
tccagctcct	taaactgacg	ctagtcaata	aacctgggca	agtgaggcaa	gagaaatgag	6060
gaagaatcca	tctgtgaggt	gacaggcacg	gatgaaagac	aaagacggaa	aagagtatca	6120
aaggcagaaa	ggagatcatt	tagttgggtc	tgaaaggaaa	agtnnttgct	atccgacatg	6180
tactgctagt	wcctgtaagc	attttaggtc	ccagaatgga	aaaaaaaaatc	aagctatngg	6240
ttatataata	atgnnnnnnn	nnnnnnnnnn	nntcgagcat	gcatctagag	ggccctattc	6300
tatagtgtca	cctaaatgct	agagctcgct	ctcagcctc	gactgtgcct	tctagttgcc	6360
agccacttgt	tgtttgcccc	tcccccgtgc	cttccctgac	cctggaagggt	gccactccca	6420
ctgtcctttc	ctaataaaaat	gaggaaattg	catcgcatgt	tctgagtagg	tgtcattcta	6480
ttctgggggg	tggggtgggg	caggacagca	agggggagga	ttgggaagac	aatagcaggc	6540
atgctgggga	tgcggtgggc	tctatggctt	ctgaggcgga	aagaaccagc	tggggctcta	6600
gggggtatcc	ccacgcgccc	tgtagcggcg	cattaagcgc	ggcgggtgtg	gtgggtacgc	6660
gcagcgtgac	cgctacactt	gccagcgccc	tagegcgcgc	tcctttcgct	ttcttccctt	6720
cctttctcgc	cacgttcgcc	ggctttcccc	gtcaagctct	aaatcggggc	atccctttag	6780
ggttccgatt	tagtgcttta	cggcacctcg	acccccaaaa	acttgattag	ggtgatggtt	6840
cacgtagtgg	gccatcgccc	tgatagacgg	tttttgcgcc	tttgacgttg	gagtcacagt	6900
tctttaatag	tggactcttg	ttccaaactg	gaacaacact	caaccctatc	tcggtctatt	6960
cttttgattt	ataagggatt	ttgggggattt	cggcctattg	gttaaaaaat	gagctgattt	7020
aacaaaaatt	taacgcgaat	tctagagccc	cgcgcgcgga	cgaactaaac	ctgactacgg	7080
catctctgcc	ccttcttcgc	ggggcagtg	atgtaatccc	ttcagttgg	tgggtacaact	7140
tgccaactgg	gccctgttcc	acatgtgaca	cgggggggga	ccaaacacaa	aggggttctc	7200
tgactgtagt	tgacatcctt	ataaatggat	gtgcacattt	gccaaactg	agtggctttc	7260
atcctggagc	agactttgca	gtctgtggac	tgcaacacaa	cattgccttt	atgtgtaact	7320
cttggctgaa	gctcttacac	caatgctggg	ggacatgtac	ctcccagggg	cccaggaaga	7380
ctacgggagg	ctacaccaac	gtcaatcaga	ggggcctgtg	tagctaccga	taagcggacc	7440
ctcaagaggg	cattagcaat	agtgtttata	aggccccctt	gttaacccta	aacgggtagc	7500
atatgcttcc	cgggtagtag	tatatactat	ccagactaac	cctaattcaa	tagcatatgt	7560
tacccaacgg	gaagcatatg	ctatcgaatt	agggttagta	aaagggtcct	aaggaacagc	7620
gatatctccc	accccatgag	ctgtcacgg	tttatttaca	tggggtcagg	attccacgag	7680
ggtagtgaac	catttttagtc	acaagggcag	tggctgaaga	tcaaggagcg	ggcagtgaa	7740
tctcctgaat	cttcgcctgc	ttcttcattc	tccttcgttt	agctaataga	ataactgctg	7800
agttgtgaac	agtaagggtg	atgtgaggtg	ctcgaaaaca	aggtttcagg	tgacgcccc	7860
agaataaaaa	ttggacgggg	ggttcagtg	tggcattgtg	ctatgacacc	aatataaacc	7920
tcacaaaccc	cttgggcaat	aaataactag	gtaggaaatga	aacattctga	atatctttta	7980
caatagaaat	ccatgggggtg	gggacaagcc	gtaaagactg	gatgtccatc	tcacacgaat	8040
ttatggctat	gggcaacaca	taatcctagt	gcaatatgat	actgggggta	ttaagatgtg	8100
tcccaggcag	ggaccaagac	aggtgaacca	tgttggttaca	ctctatttgt	aacaagggga	8160
aagagagtgg	acgcccagac	cagcggactc	cactgggtgt	ctctaaccac	cccgaaaatt	8220
aaacggggct	ccacgccaat	ggggcccata	aacaaagaca	agtgggccact	cttttttttg	8280

aaattgtgga	gtggggggcac	gcgtcagccc	ccacacgccc	ccctgcgggtt	ttggactgta	8340
aaataagggg	gtaataactt	ggctgattgt	aaccccgcga	accactgcgg	tcaaaccact	8400
tgccacaaa	accactaatg	gcaccccg	gaatacctgc	ataagtaggt	gggccccca	8460
agataggggc	gcgattgctg	cgatctggag	gacaaattac	acacacttgc	gcctgagcgc	8520
caagcacagg	gttgttggtc	ctcatattca	cgaggtcgct	gagagcacgg	tgggctaata	8580
ttgccatggg	tagcatatac	tacccaaata	tctggatagc	atatgctatc	ctaatactata	8640
tctgggtagc	ataggctatc	ctaatactata	tctgggtagc	atatgctatc	ctaatactata	8700
tctgggtagt	atatgctatc	ctaatttata	tctgggtagc	ataggctatc	ctaatactata	8760
tctgggtagc	atatgctatc	ctaatactata	tctgggtagt	atatgctatc	ctaatactgta	8820
tccgggtagc	atatgctatc	caaatactat	ttagggtagt	atatgctatc	ctaatttata	8880
tctgggtagc	atatgctatc	caaatactat	gtagcatat	gctatcctaa	tctatatctg	8940
ggtagcatat	gctatcctaa	tctatatctg	gtagcatag	gctatcctaa	tctatatctg	9000
ggtagcatat	gctatcctaa	tctatatctg	gtagtatat	gctatcctaa	tttatatctg	9060
ggtagcatag	gctatcctaa	tctatatctg	gtagcatat	gctatcctaa	tctatatctg	9120
ggtagtatat	gctatcctaa	tctgtatccg	gtagcatat	gctatcctca	tgcataatac	9180
gtcagcatat	gataccaggt	agtagagtgg	gagtgcctatc	ctttgcatat	gccgccacct	9240
cccaaggggg	cgtgaatttt	cgctgcttgt	cccttttctg	catgctgggt	gctcccatc	9300
ttaggtgaat	ttaaggaggc	caggctaaag	ccgtcgcagt	tctgattgct	caccaggtaa	9360
atgtcgctaa	tgttttccaa	cgcgagaagg	tgttgagcgc	ggagctgagt	gacgtgacaa	9420
catgggtatg	cccaattgcc	ccatgttggg	aggacgaaaa	tgggtgacaag	acagatggcc	9480
agaaatacac	caacagcacg	catgatgtct	actgggggatt	tattcttttag	tgcgggggaa	9540
tacacggctt	ttaatacgat	tgaggggcgtc	tcctaacaag	ttacatcaact	cctgcccttc	9600
ctcaccctca	tctccatcac	ctccttcac	tcctgcctct	ccgtcatcac	cctccgcggc	9660
agcccttcc	accataggtg	gaaaccaggg	aggcaaatct	actccatcgt	caaagctgca	9720
cacagtcacc	ctgatattgc	aggtaggagc	gggtcttgtc	ataacaagggt	ccttaatcgc	9780
atccttcaaa	acctcagcaa	atatatgagt	ttgtaaaaag	accatgaaat	aacagacaat	9840
ggactccctt	agcggggccag	gttgtggggc	gggtccaggg	gccattccaa	aggggagacg	9900
actcaatggg	gtaagacgac	attgtggaat	agcaagggca	gttctctgcc	ttaggttgta	9960
aagggagggt	ttactacctc	catatacgaa	cacaccggcg	acccaagtct	cttgcgtcgg	10020
agtcctttct	acgtgactcc	tagccaggag	agctcttaaa	ccttctgcaa	tgttctcaaa	10080
tttgcgggtg	gaacctcctt	gaccacgatg	ctttccaaac	cacctcctt	ttttgcgcct	10140
gcctccatca	ccctgacccc	gggtccaggt	gcttgggcct	tctcctgggt	catctgcggg	10200
gccctgctct	atcgctcccc	ggggcacgtc	aggctcacca	tctggggccac	cttcttggtg	10260
gtattcaaaa	taatcggctt	cccctacagg	gtggaaaaat	ggccttctac	ctggaggggg	10320
cctgcgcggg	ggagaccggg	atgatgatga	ctgactactg	ggactcctgg	gcctcttttc	10380
tccacgtcca	cgacctctcc	ccctggctct	ttcacgactt	ccccccctgg	ctctttcacg	10440
tccctctacc	cggcggcctc	cactacctcc	tcgaccctgg	cctccactac	ctcctcgacc	10500
cggcctcca	ctgcctcctc	gaccccgggc	tccacctcct	gctcctgccc	ctcctgctcc	10560
tgcctcctct	cctgctcctg	cccctcctgc	ccctcctgct	cctgcccctc	ctgcccctcc	10620
tgtcctgccc	cctcctgccc	ctcctgctcc	tgcctcctct	gcccctcctc	ctgctcctgc	10680
ccctcctgccc	cctcctcctg	ctcctgcccc	tccctgcccct	cctgctcctg	cccctcctgc	10740
ccctcctgct	cctgcccctc	ctgcccctcc	tgtcctgccc	cctcctgctc	ctgcccctcc	10800
tgtcctgccc	cctcctgctc	ctgcccctcc	tgcccctcct	gcccctcctc	ctgctcctgc	10860
ccctcctgct	cctgcccctc	ctgcccctcc	tgcccctcct	gctcctgccc	ctcctcctgc	10920
tccctgcccct	cctgcccctc	ctgcccctcc	tccctgcccct	gcccctcctg	cccctcctcc	10980
tgtcctgccc	cctcctcctg	ctcctgcccc	cctgcccctc	cctgcccctc	ctcctgctcc	11040
tgcctcctcc	gcccctcctc	ctcctcctgc	ccctcctcct	gctcctgccc	ctcctgcccc	11100
tccctgcccct	cctcctgctc	ctgcccctcc	tccctgctcc	gcccctcctg	cccctcctgc	11160
ccctcctgccc	cctcctcctg	ctcctgcccc	tccctgctcc	cctgcccctc	ctgctcctgc	11220
ccctcccgt	cctgctcctg	ctcctgttcc	accgtgggtc	cctttgcagc	caatgcaact	11280
tggacgtttt	tgggggtctcc	ggacaccatc	tctatgtctt	ggccctgatc	ctgagccggc	11340
cgggggtcct	ggtcttccgc	ctcctcgctc	tcgtcctctt	ccccgtcctc	gtccatgggt	11400
atcacccctt	cttcttttag	gtccactgcc	gccggagcct	tctggtccag	atgtgtctcc	11460
cttctctcct	aggccatttc	caggctcctg	acctggcccc	tcgtcagaca	tgattcacac	11520
taaaagagat	caatagacat	ctttattaga	cgacgctcag	tgaatacagg	gagtgcagac	11580
tccctgcccc	tccaacagcc	ccccaccct	catccccctc	atggctcgtg	tcagacagat	11640
ccagggtctga	aaattcccca	tccctccgaac	catcctcgctc	ctcatcacca	attactcgca	11700
gccccgaaaa	ctcccgtgta	acatcctcaa	gatttgctgc	ctgagcctca	agccaggcct	11760
caaattcctc	gtcccccttt	ttgctggacg	gtagggatgg	ggattctcgg	gacccctcct	11820
cttctctctt	aagggtcacca	gacagagatg	ctactggggc	aacggaagaa	aagctgggtg	11880
cggcctgtga	ggatcagctt	atcgatgata	agctgtcaaa	catgagaatt	cttgaagacg	11940

aaagggcctc	gtgatacgcc	tatTTTTata	ggTtaatgtc	atgataataa	tggTttctta	12000
gacgtcaggt	ggcactTTTc	ggggaaatgt	gcgcggaacc	cctattTgtt	tatTTTTcta	12060
aatacattca	aatatgtatc	cgctcatgag	acaataaccc	tgataaatgc	ttcaataata	12120
ttgaaaaagg	aagagtatga	gtattcaaca	tttccgtgtc	gcccttatTc	cctTTTTtgc	12180
ggcattTTTgc	cttccTgttt	ttgctcaccC	agaaacgctg	gtgaaagtaa	aagatgctga	12240
agatcagttg	ggTgcacgag	tgggttacat	cgaactggat	ctcaacagcg	gtaagatcct	12300
tgagagTTTT	cgccccgaag	aacgTTTTTc	aatgatgagc	actTTTaaag	ttctgctatg	12360
tgggcgcggt	ttatcccgTg	ttgacgcggg	gcaagagcaa	ctcggtcgcc	gcatacacta	12420
ttctcagaat	gactTggTtg	agtactcacc	agtcacagaa	aagcatctta	cggatggcat	12480
gacagtaaga	gaattatgca	gtgctgccat	aaccatgagt	gataaacactg	cggccaactt	12540
acttctgaca	acgatcgag	gaccgaagga	gctaaccgct	TTTTTgcaca	acatggggga	12600
tcattgtaact	cgccTtgatc	gttgggaacc	ggagctgaat	gaagccatac	caaacgcacga	12660
gcgtgacacc	acgatgcctg	cagcaatggc	aacaacgttg	cgcaaactat	taactggcga	12720
actacttact	ctagcttccc	ggcaacaatt	aatagactgg	atggaggcgg	ataaagttgc	12780
aggaccactt	ctgcgctcgg	cccttccggc	tggctggTtt	attgctgata	aatctggagc	12840
cggtgagcgt	gggtctcgcg	gtatcattgc	agcactgggg	ccagatggta	agccctcccg	12900
tatcgtagtt	atctacacga	cggggagTca	ggcaactatg	gatgaacgaa	atagacagat	12960
cgctgagata	ggTgcctcac	tgattaaagca	ttgTtaactg	tcagaccaag	tttactcata	13020
tatactTTtag	attgattTaa	aacttcatTT	ttaattTaaa	aggatctagg	tgaagatcct	13080
TTTTgataat	ctcatgacca	aaatccctta	acgtgagTtt	tcgttccact	gagcgtcaga	13140
ccccgtagaa	aagatcaaag	gatcttcttg	agatccTTTT	tttctgcgcg	taatctgctg	13200
cttgcaaaca	aaaaaaccac	cgctaccagc	ggTggTttgt	ttgcgggatc	aagagctacc	13260
aactctTTTT	ccgaaggtaa	ctggcttcag	cagagcgcag	ataccaaata	ctgtccttct	13320
agtgtagccg	tagttaggcc	accacttcaa	gaactctgta	gcaccgccta	cataacctcg	13380
tctgctaata	ctgttaccag	tggctgctgc	cagtggcgat	aagtctgttc	ttaccgggtt	13440
ggactcaaga	cgatagtTtac	cggataaggc	gcagcggTcg	ggctgaacgg	ggggTtcgtg	13500
cacacagccc	agctTggagc	gaacgaccta	caccgaactg	agatacctac	agcgtgagct	13560
atgagaaagc	gccacgcttc	ccgaagggag	aaaggcggag	aggTatccgg	taagcggcag	13620
ggtcggaaca	ggagagcgca	cgaggggagc	tccaggggga	aacgcctggt	atctttatag	13680
tctgtcgggg	tttcgccacc	tctgacttga	gcgtcgattt	ttgtgatgct	cgtcaggggg	13740
gcggagccta	tggaaaaacg	ccagcaacgc	ggcctTTTTa	cggttccctg	ccttttgctg	13800
cgccgcgtgc	ggctgctgga	gatggcggac	gcgatggata	tgTtctgcca	agggttggtt	13860
tgcgcaattca	cagTtctccg	caagaattga	ttggctccaa	ttcttgagTg	ggtgaatccg	13920
ttagcgaggt	gccgcgggct	tccattcagg	tcgaggtggc	ccggctccat	gcaccgcgac	13980
gcaacgcggg	gaggcagaca	aggTataggg	cggcgccctac	aatccatgcc	aaccggTtcc	14040
atgtgctcgc	cgaggcggca	taaatcgccg	tgacgatcag	cggtccagTg	atcgaagTta	14100
ggctggtaag	agccgcgagc	gacTcttgaa	gctgtccctg	atggtcgtca	tctacTgTcc	14160
tgacagcat	ggcctgcaac	gcgggcattc	cgatgccggc	ggaagcgaga	agaatcataa	14220
tggggaaggc	catccagcct	cgcgTcgcg	acgccagcaa	gacgtagccc	agcgcgtcgg	14280
ccgccatgcc	ctgcttcac	cccgTggccc	gttgctcgcg	tttgcTggcg	gtgtccccgg	14340
aagaaatata	tttgcatgtc	tttagTtcta	tgatgacaca	aaccccgccc	agcgtctTgt	14400
cattggcgaa	ttcgaacacg	cagatgcagT	cggggcggcg	cggtcccagg	tccactTcgc	14460
atattaaggt	gacgcgtgtg	gcctcgaaaca	ccgagcgacc	ctgcagcgac	ccgcttaaca	14520
gcgtcaacag	cgtgccgcag	atcccgggca	atgagatatg	aaaaagcctg	aactcaccgc	14580
gacgtctgtc	gagaagTttc	tgatcgaaaa	gttcgacagc	gtctccgacc	tgatgcagct	14640
ctcggagggc	gaagaatctc	gtgctttcag	cttcgatgta	ggagggcgtg	gatatgtcct	14700
gcgggtaaat	agctgcgcgg	atggTttcta	caaagatcgt	tagtgggatc	ggcactTtgc	14760
atcgcccgcg	ctccccgatt	ccggaagtgc	ttgacattgg	ggaattcagc	gagagcctga	14820
cctattgcat	ctcccgccgt	gcacagggtg	tcacgtTgca	agacctgcct	gaaaccgaac	14880
tgcccgctgt	tctgcagccg	gtcgcggagg	ccatggatgc	gatcgctgcg	gccgatctta	14940
gccagacgag	cgggttcggc	ccattcggac	cgcaagggaat	cggtcaatac	actacatggc	15000
gtgatttcat	atgcgcgatt	gctgatcccc	atgtgtatca	ctggcaaact	gtgatggacg	15060
acaccgtcag	tgcgTccgtc	gcgcaggctc	tcgatgagct	gatgctTtgg	gccgaggact	15120
gccccgaagt	ccggcacctc	gtgcacgcgg	atttcggctc	caacaatgtc	ctgacggaca	15180
atggccgcat	aacagcggtc	attgactgga	cgaggcgcat	gttcggggat	tcccaatacg	15240
aggTcgccaa	catcttcttc	tggaggccgt	ggTtggcggg	tatggagcag	cagacgcgct	15300
acttcgagcg	gaggcatccg	gagcttgca	gatcgccgcg	gctccggggc	tatatgctcc	15360
gcattggTct	tgaccaactc	tatcagagct	tggTtgacgg	caatttcgat	gatgcagctt	15420
gggcgcaggg	tcgatgcgac	gcaatcgTcc	gatccggagc	cgggactgtc	gggcgtacac	15480
aaatcgcccc	cagaagcgcg	gccgtctgga	ccgatggctg	tgtagaagta	ctcgccgata	15540
gtggaaacgg	gagatggggg	aggctaactg	aaacacggaa	ggagacaata	ccggaaggaa	15600

```

ccccgcgtat gacggcaata aaaagacaga ataaaacgca cgggtggttg gtcgtttgtt 15660
cataaacgcg ggggttcggtc ccagggctgg cactctgtcg ataccccacc gagaccccat 15720
tggggccaat acgcccgcgt ttcttccttt tccccacccc acccccacag ttcgggtgaa 15780
ggcccagggc tcgcagccaa cgtcggggcg gcaggccctg ccatagccac tggccccgtg 15840
ggttagggac ggggtccccc atggggaatg gtttatggtt cgtggggggtt attattttgg 15900
gcgttgctg gggctctggc cacgactgga ctgagcagac agacccatgg tttttggatg 15960
gcctgggcat ggaccgcatg tactggcgcg acacgaacac cgggcgtctg tggctgccaa 16020
acacccccga cccccaaaaa ccaccgcgcg gatttctggc gtgccaagct agtcgaccaa 16080

```

```

<210> 49
<211> 32
<212> DNA
<213> Homo sapiens

```

```

<400> 49
ccccgccgga ggggcagctt tgtggagatg gt 32

```

```

<210> 50
<211> 11
<212> PRT
<213> Homo sapiens

```

```

<400> 50
Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
1           5           10

```

```

<210> 51
<211> 5
<212> PRT
<213> Homo sapiens

```

```

<400> 51
Val Asn Leu Asp Ala
1           5

```

```

<210> 52
<211> 9
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic oligopeptide substrate

```

```

<400> 52
Ser Glu Val Asn Leu Asp Ala Glu Phe
1           5

```

```

<210> 53
<211> 30
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic oligopeptide substrate

```

```

<400> 53
Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile
1           5           10           15

```

1922075460

Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu Phe
 20 25 30

<210> 54
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Wild type Amyloid Precursor Protein cleavage site
 (fragment)

<400> 54
 Val Lys Met Asp Ala
 1 5

<210> 55
 <211> 24
 <212> PRT
 <213> Homo sapiens

<400> 55
 Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
 1 5 10 15
 Glu Met Val Asp Asn Leu Arg Gly
 20

<210> 56
 <211> 15
 <212> PRT
 <213> Homo sapiens

<400> 56
 Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg
 1 5 10 15

<210> 57
 <211> 419
 <212> PRT
 <213> Homo sapiens

<400> 57
 Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15
 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30
 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45
 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile

2024-04-04 15:43:59

145 150 155 160
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205
 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220
 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365
 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380
 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415
 Val Ser Ala

<210> 58
 <211> 407
 <212> PRT
 <213> Homo sapiens

<400> 58
 Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
 1 5 10 15
 Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val
 20 25 30
 Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
 35 40 45
 Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
 50 55 60
 His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
 65 70 75 80
 Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
 85 90 95
 Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg
 100 105 110
 Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
 115 120 125
 Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg
 130 135 140
 Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr

145 150 155 160
 His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro
 165 170 175
 Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile
 180 185 190
 Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro
 195 200 205
 Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile
 210 215 220
 Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys
 225 230 235 240
 Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val
 245 250 255
 Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys
 260 265 270
 Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala
 275 280 285
 Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met
 290 295 300
 Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln
 305 310 315 320
 Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr
 325 330 335
 Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val
 340 345 350
 Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
 355 360 365
 Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala
 370 375 380
 Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr
 385 390 395 400
 Asn Ile Pro Gln Thr Asp Glu
 405

<210> 59

<211> 452

<212> PRT

<213> Homo sapiens

<400> 59

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15
 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30
 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45
 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp

165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205
 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220
 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365
 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380
 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415
 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
 420 425 430
 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
 435 440 445
 Gln Thr Asp Glu
 450

<210> 60
 <211> 420
 <212> PRT
 <213> Homo sapiens

<400> 60
 Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15
 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30
 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45
 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp

130 135 140
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205
 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220
 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365
 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380
 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415
 Val Ser Ala Cys
 420

<210> 61

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide inhibitor

<221> MOD_RES

<222> 4

<223> Xaa = hydroxyethylene

<400> 61

Glu Val Met Xaa Ala Glu Phe
 1 5

<210> 62

<211> 26

<212> PRT

<213> Homo sapiens

<400> 62

Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met

1 5 10 15
 Leu Pro Leu Cys Leu Met Val Cys Gln Trp
 20 25

<210> 63
 <211> 33
 <212> PRT
 <213> Homo sapiens

<220>
 <223> P26-P4'sw peptide substrate

<400> 63
 Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu
 1 5 10 15
 Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu
 20 25 30
 Phe

<210> 64
 <211> 29
 <212> PRT
 <213> Homo sapiens

<220>
 <223> P26-P1' peptide substrate with CGG linker

<400> 64
 Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu
 1 5 10 15
 Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu
 20 25

<210> 65
 <211> 501
 <212> PRT
 <213> Mus musculus

<400> 65
 Met Ala Pro Ala Leu His Trp Leu Leu Leu Trp Val Gly Ser Gly Met
 1 5 10 15
 Leu Pro Ala Gln Gly Thr His Leu Gly Ile Arg Leu Pro Leu Arg Ser
 20 25 30
 Gly Leu Ala Gly Pro Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 35 40 45
 Glu Glu Ser Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 50 55 60
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 65 70 75 80
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 85 90 95
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 100 105 110
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 115 120 125
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 130 135 140
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 145 150 155 160
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp

165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro
 195 200 205
 Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220
 Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365
 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380
 Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415
 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
 420 425 430
 Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
 435 440 445
 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
 450 455 460
 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
 465 470 475 480
 Arg Cys Leu Arg Cys Leu Arg His Gln His Asp Asp Phe Gly Asp Asp
 485 490 495
 Ile Ser Leu Leu Lys
 500

<210> 66

<211> 480

<212> PRT

<213> Homo sapiens

<400> 66

Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
 1 5 10 15
 Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu
 20 25 30
 Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly
 35 40 45
 Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro
 50 55 60
 Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val
 65 70 75 80
 Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu

85 90 95
 Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr
 100 105 110
 Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro
 115 120 125
 His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu
 130 135 140
 Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly
 145 150 155 160
 Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Ser Leu Glu Pro Phe
 165 170 175
 Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu
 180 185 190
 Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala
 195 200 205
 Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr
 210 215 220
 Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu
 225 230 235 240
 Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp
 245 250 255
 Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr
 260 265 270
 Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile
 275 280 285
 Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly
 290 295 300
 Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe
 305 310 315 320
 Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
 325 330 335
 Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val
 340 345 350
 Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser
 355 360 365
 Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val
 370 375 380
 Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
 385 390 395 400
 Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr
 405 410 415
 Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
 420 425 430
 Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe
 435 440 445
 Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys
 450 455 460
 Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
 465 470 475 480

<210> 67

<211> 444

<212> PRT

<213> Homo sapiens

<400> 67

Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln
 1 5 10 15
 Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn
 20 25 30

09704574.071704
 1022074574.071704

Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro
 35 40 45
 His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr
 50 55 60
 Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp
 65 70 75 80
 Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn
 85 90 95
 Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe
 100 105 110
 Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala
 115 120 125
 Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu
 130 135 140
 Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly
 145 150 155 160
 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 165 170 175
 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 180 185 190
 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 195 200 205
 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 210 215 220
 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 225 230 235 240
 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 245 250 255
 Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
 260 265 270
 Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 275 280 285
 Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 290 295 300
 Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 305 310 315 320
 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 325 330 335
 Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
 340 345 350
 Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
 355 360 365
 Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
 370 375 380
 Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr
 385 390 395 400
 Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
 405 410 415
 Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln
 420 425 430
 His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
 435 440

<210> 68

<211> 395

<212> PRT

<213> Homo sapiens

<400> 68

Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln
 1 5 10 15

0972421-03704
 T02421-03704

Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn
 20 25 30
 Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro
 35 40 45
 His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr
 50 55 60
 Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp
 65 70 75 80
 Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn
 85 90 95
 Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe
 100 105 110
 Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala
 115 120 125
 Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu
 130 135 140
 Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly
 145 150 155 160
 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
 165 170 175
 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
 180 185 190
 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
 195 200 205
 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
 210 215 220
 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
 225 230 235 240
 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
 245 250 255
 Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
 260 265 270
 Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
 275 280 285
 Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
 290 295 300
 Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
 305 310 315 320
 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
 325 330 335
 Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
 340 345 350
 Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
 355 360 365
 Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
 370 375 380
 Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
 385 390 395

<210> 69

<211> 439

<212> PRT

<213> Homo sapiens

<400> 69

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
 1 5 10 15
 Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
 20 25 30
 Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
 35 40 45

0924431-074704
 T02720 T044260

Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
 50 55 60
 Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
 65 70 75 80
 Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
 85 90 95
 Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser
 100 105 110
 Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
 115 120 125
 Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
 130 135 140
 Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
 145 150 155 160
 Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
 165 170 175
 Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
 180 185 190
 Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
 195 200 205
 Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
 210 215 220
 Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
 225 230 235 240
 Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
 245 250 255
 Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
 260 265 270
 Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
 275 280 285
 Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
 290 295 300
 Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
 305 310 315 320
 Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
 325 330 335
 Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
 340 345 350
 Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
 355 360 365
 Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
 370 375 380
 Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met
 385 390 395 400
 Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys
 405 410 415
 Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala
 420 425 430
 Asp Asp Ile Ser Leu Leu Lys
 435

<210> 70

<211> 390

<212> PRT

<213> Homo sapiens

<400> 70

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
 1 5 10 15
 Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
 20 25 30

Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
 35 40 45
 Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
 50 55 60
 Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
 65 70 75 80
 Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
 85 90 95
 Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser
 100 105 110
 Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
 115 120 125
 Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
 130 135 140
 Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
 145 150 155 160
 Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
 165 170 175
 Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
 180 185 190
 Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
 195 200 205
 Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
 210 215 220
 Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
 225 230 235 240
 Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
 245 250 255
 Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
 260 265 270
 Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
 275 280 285
 Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
 290 295 300
 Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
 305 310 315 320
 Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
 325 330 335
 Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
 340 345 350
 Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
 355 360 365
 Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
 370 375 380
 Ile Pro Gln Thr Asp Glu
 385 390

<210> 71

<211> 374

<212> PRT

<213> Homo sapiens

<400> 71

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
 1 5 10 15
 Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val
 20 25 30
 Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
 35 40 45
 Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
 50 55 60

His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
 65 70 75 80
 Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
 85 90 95
 Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg
 100 105 110
 Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
 115 120 125
 Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg
 130 135 140
 Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr
 145 150 155 160
 His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro
 165 170 175
 Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile
 180 185 190
 Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro
 195 200 205
 Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile
 210 215 220
 Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys
 225 230 235 240
 Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val
 245 250 255
 Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys
 260 265 270
 Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala
 275 280 285
 Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met
 290 295 300
 Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln
 305 310 315 320
 Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr
 325 330 335
 Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val
 340 345 350
 Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
 355 360 365
 Gly Phe Ala Val Ser Ala
 370

<210> 72

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> P10-P4'staD-V peptide inhibitor

<221> MOD_RES

<222> 10

<223> Xaa is statine moiety

<400> 72

Lys Thr Glu Glu Ile Ser Glu Val Asn Xaa Val Ala Glu Phe
 1 5 10

<210> 73

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> P4-P4'staD-V peptide inhibitor

<221> MOD_RES

<222> 5

<223> Xaa is statine moiety

<400> 73

Ser Glu Val Asn Xaa Val Ala Glu Phe

1

5

<210> 74

<211> 431

<212> PRT

<213> Homo sapiens

<400> 74

Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
 1 5 10 15
 Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu
 20 25 30
 Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly
 35 40 45
 Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro
 50 55 60
 Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val
 65 70 75 80
 Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu
 85 90 95
 Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr
 100 105 110
 Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro
 115 120 125
 His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu
 130 135 140
 Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly
 145 150 155 160
 Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe
 165 170 175
 Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu
 180 185 190
 Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala
 195 200 205
 Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr
 210 215 220
 Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu
 225 230 235 240
 Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp
 245 250 255
 Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr
 260 265 270
 Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile
 275 280 285
 Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly
 290 295 300
 Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe
 305 310 315 320
 Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
 325 330 335
 Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val

09704571.071704

			340					345				350			
Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser
		355					360					365			
Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val
	370					375					380				
Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His
385					390				395					400	
Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	Thr
			405					410					415		
Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu	
		420						425					430		

<210> 75

<211> 361

<212> PRT

<213> Homo sapiens

<400> 75

Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu
1			5					10						15	
Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr
		20					25					30			
Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His
	35					40					45				
Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys
50					55					60					
Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly
65				70					75					80	
Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala
			85					90					95		
Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser
		100					105					110			
Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro
	115					120					125				
Asp	Asp	Ser	Leu	Glu	Pro	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	
130					135					140					
Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu
145				150						155				160	
Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly
			165					170					175		
Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile
	180						185					190			
Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn
	195					200					205				
Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser
	210				215						220				
Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe
225				230						235				240	
Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe
			245					250					255		
Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly
	260					265						270			
Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly
	275				280						285				
Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr
	290				295						300				
Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys
305				310						315				320	
Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile
			325					330					335		
Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly

F02720.T642460

340 345 350
 Phe Ala Val Ser Ala Cys His Val His
 355 360

<210> 76
 <211> 63
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(63)
 <223> n = A,T,C or G

<400> 76
 garacngayg argarcnga rgarcnggn mgnmgnggnw snttygtnga ratggtn gay 60
 aay 63

<210> 77
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 77
 Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
 1 5 10 15
 Glu Met Val Asp Asn
 20

<210> 78
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide inhibitor P3-P4' XD-V
 <221> MOD_RES
 <222> 3
 <223> Xaa is hydroxyethylene or statine

<400> 78
 Val Met Xaa Val Ala Glu Phe
 1 5

<210> 79
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 79
 Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
 1 5 10

<210> 80
 <211> 419
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotide insert in vector pCF

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100

```
<210> 81
<211> 8
<212> PRT
<213> Artificial Sequence
```

```
<400> 81
Glu Val Met Xaa Val Ala Glu Phe
 1             5
```

<220>
<223> APP fragment P5-P4' wt

```
<210> 83
<211> 9
<212> PRT
<213> Homo sapiens
```

```
<400> 83
Ser Glu Val Asn Leu Asp Ala Glu Phe
  1             5
```

```
<220>
<223> APP fragment
```

```
<400> 84
Ser Glu Val Lys Leu Asp Ala Glu Phe
  1             5
```

<210> 85
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 85
Ser Glu Val Lys Phe Asp Ala Glu Phe
1 5

<210> 86
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 86
Ser Glu Val Asn Phe Asp Ala Glu Phe
1 5

<210> 87
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 87
Ser Glu Val Lys Met Ala Ala Glu Phe
1 5

<210> 88
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 88
Ser Glu Val Asn Leu Ala Ala Glu Phe
1 5

<210> 89
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 89
Ser Glu Val Lys Leu Ala Ala Glu Phe
1 5

```

<210> 90
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 90
Ser Glu Val Lys Met Leu Ala Glu Phe
  1                      5

<210> 91
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 91
Ser Glu Val Asn Leu Leu Ala Glu Phe
  1                      5

<210> 92
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 92
Ser Glu Val Lys Leu Leu Ala Glu Phe
  1                      5

<210> 93
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 93
Ser Glu Val Lys Phe Ala Ala Glu Phe
  1                      5

<210> 94
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> APP fragment

<400> 94
Ser Glu Val Asn Phe Ala Ala Glu Phe
  1                      5

<210> 95

```

<211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> APP fragment

<400> 95
 Ser Glu Val Lys Phe Leu Ala Glu Phe
 1 5

<210> 96
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> APP fragment

<400> 96
 Ser Glu Val Asn Phe Leu Ala Glu Phe
 1 5

<210> 97
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> APP-derived fragment P10-P4' (D-V)

<400> 97
 Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Val Ala Glu Phe
 1 5 10

<210> 98
 <211> 35
 <212> DNA
 <213> Homo sapiens

<400> 98
 cccgaggagc ccggccggag gggcagcttt gtcga

35

<210> 99
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 99
 Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg
 1 5 10

<210> 100
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant 293T cells

<400> 100

09440749460

Thr Gln His Gly Ile Arg Leu Pro Leu Arg
 1 5 10

<210> 101

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant 293T cells

<400> 101

Met Val Asp Asn Leu Arg Gly Lys Ser
 1 5

<210> 102

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant CosA2 cells

<400> 102

Gly Ser Phe Val Glu Met Val Asp Asn Leu
 1 5 10

<210> 103

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> APP substrate fragment:WT Sequence

<400> 103

Val Lys Met Asp
 1

<210> 104

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> APP substrate fragment:Swedish Sequence

<400> 104

Val Asn Leu Asp
 1